

Alpha Viruses nsp2 alignment

CLUSTAL W (1.82) multiple sequence alignment

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SFV_nsp2      GVVETPRSALKVTAQPNVDVLLGNYVVLSPQTVLKSSKLAPVHPLAEQVKIITHNGRAGGY 60
RRV_nsp2      GVVETPRNALKVTPQERDQLIGAYLILSPQTVLKSEKLTPIHPLAEQVTIMTHSGRSGRY 60
ONV_nsp2      GIVETPRGAIKVTAQPSDLVVGEYLVLTPOAVLRSQKLSLIHALAEQVKTCTHSGRAGRY 60
SinV_nsp2     ALVETPRGHVRIIPQANDRMIGQYIVVSPNSVLKNAKLAPAHPLADQVKIITHSGRSGRY 60
VEEV_nsp2     GSVETPRGLIKVTSYAGEDKIGSYAVLSPQAVLKSEKLSLHPLAEQVIVITHSGRKGRY 60
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SFV_nsp2      QVDGYDGRVLLPCGSAIPVPEFQALSESATMVYNEREFVNRKLYHIAVHGPSLNTDEENY 120
RRV_nsp2      PVDRYDGRVLVPTGAAIPVSEFQALSESATMVYNEREFINRKLHHIALYGPALNTDEENY 120
ONV_nsp2      AVEAYDGRVLVPSGYAIPQEDFQSLSESATMVNEREFVNRKLHHIAMHGPAALNTDEESY 120
SinV_nsp2     AVEPYDAKVLMPAGGAVPWPEFLALSESATLVYNEREFVNRKLYHIAMHGPAKNTDEEEQY 120
VEEV_nsp2     AVEPYHGKVVVPEGHAIPVQDFQALSESATIVYNEREFVNRYLHHIATHGGALNTDEEYY 120
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SFV_nsp2      EKVRAERTDAEYVFDVDDKKCCVKREEASGLVLVGELTNPPFHEFAYEGLKIRPSAPYKTT 180
RRV_nsp2      EKVRAERAEEYVFDVDDKRTCVKREDASGLVLVGDLINPPFHEFAYEGLKIRPATPFQTT 180
ONV_nsp2      ELVRVEKTEHEYVYDVDQKKCKKREEATGLVLVGDLTSPPYHEFAYEGLKIRPACPYKTA 180
SinV_nsp2     KVTKAELAETHEYVFDVDDKRCVKKEEASGLVLSGELTNPPYHELALEGLKTRPAVPYKVE 180
VEEV_nsp2     KTVKPSEHDGEYLYDIDRKQCVKKELVTGLGLTGELVDPPFHEFAYESLRTRPAAPYQVP 180
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SFV_nsp2      VVGVEFGVPGSGKSAIIKSLVTKHDLVTSGKKENCQEIVNDVKKHRGKGTRENSDSILLN 240
RRV_nsp2      VIGVEFGVPGSGKSAIIKSVVTTLDLVASGKKENCQEIVNDVKKQRGLDVTARTVDSILLN 240
ONV_nsp2      VIGVEFGVPGSGKSAIIKSLVTRQDLVTSGKKENCQEISNDVMRQRKLEISARTVDSILLN 240
SinV_nsp2     TIGVIGTPGSGKSAIIKSTVTARDLVTSGKKENCREIEADVLRRLRGMQITSKTVDSVMLN 240
VEEV_nsp2     TIGVYGVPGSGKSGIIKSAVTKKDLVVSAKKENCAEIIIRDVKKMKGLDVNARTVDSVLLN 240
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SFV_nsp2      GCRRAVDILYVDEAFACHSGTLLALIALVKPRSKVVLGCDPKQCGFFNMMQLKVNFNH-- 298
RRV_nsp2      GCRRGVENLYVDEAFACHSGTLLALIAMVKPTGKVILCGDPKQCGFFNLMQLKVNFNH-- 298
ONV_nsp2      GCNKPVEVLYVDEAFACHSGTLLALIAMVRPRQKVVLGCDPKQCGFFNMMQMKVNYNH-- 298
SinV_nsp2     GCHKAVEVLYVDEAFACHAGALLALIAIVRPRKKVVLGCDPMQCGFFNMMQLKVHFNHPE 300
VEEV_nsp2     GCKHPVETLYIDEAFACHAGTLRALIAIIRPK-KAVLCGDPKQCGFFNMMCLKVHFNH-- 297
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SFV_nsp2      -NICTEVCHKSISRRCRTPVTAIVSTLHYGGKMRRTNPNCKPIIIDTTGQTKPKPGDIVL 357
RRV_nsp2      -DICTQVLHKSISRRCRLPITAIVSTLHYQGKMRRTNLCSAPIQIDTTGTTKPAKGDIVL 357
ONV_nsp2      -NICTQVYHKSISRRCRLPITAIVSSLHYESKMRRTNEYNQPIVVDTTGITKPEPGDLVL 357
SinV_nsp2     KDICTKTFYKYISRRCRTPVTAIVSTLHYDGKMKTTNPCKKNIEIDITGATKPKPGDIIL 360
VEEV_nsp2     -EICTQVFHKSISRRCRKSVTSSVSTLFDYDKMRRTNPKETKIVIDTTGSTKPKQDDLIL 356
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SFV_nsp2      TCFRGWAKQLQLDYRGHEVMTAAASQGLTRKGVYAVRQKVNENPLYAPASEHVNVLTRT 417
RRV_nsp2      TCF--WVKQLQIDYRGHEVMTAAASQGLTRKGVYAVRQKVNENPLYAPASSEHVNVLTRT 415
ONV_nsp2      TCFRGWVKQLQIDYRGNEVMTAAASQGLTRKGVYAVRQKVNENPLYAPTSEHVNVLTRT 417
SinV_nsp2     TCFRGWVKQLQIDYPGHEVMTAAASQGLTRKGVYAVRQKVNENPLYAITSEHVNVLTRT 420
VEEV_nsp2     TCFRGWVKQLQIDYKGNEIMTAAASQGLTRKGVYAVRYKVNENPLYAPTSEHVNVLTRT 416
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SFV_nsp2      EDRLVWKTLAGDPWIKVLSNIPQGNFTATLEEWQEEHDKIMKVIEGPAAPVDAFQNKANV 477
RRV_nsp2      ENRLVWKTLSGDPWIKVLTNIPKGDFSATLEEWQEEHDNIMNALRERSTAVDPFQNKAKV 475
ONV_nsp2      EGKLTWKTLSGDPWIKILQNPPKGDFAKTIKEWEAEHASIMAGICNHQMAFDTFQNKANV 477
SinV_nsp2     EDRLVWKTLSGDPWIKQPTNIPKGNFQATIEDWEAEHKGIIAAINSPTFRANPFCKNTN 480
VEEV_nsp2     EDRLVWKTLAGDPWIKILTAKYPGNFTATIEEWQAEHDAIMRHILERPDPTDVFQNKANV 476
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SFV_nsp2      CWAKSLVPVLDTAGIRLTAEWSTIITAFKEDRAYSPVVALNEICTKYGVDLDSGLFSA 537
RRV_nsp2      CWAKCLVQVLETAGIRMTAEWDTVL-AFREDRAYSPEVALNEICTKYGVDLDSGLFSA 534
ONV_nsp2      CWAKCLVPILDTAGIKLSDRQWSQIVQAFKEDRAYSPEVALNEICTRIYGVDLDSGLFSK 537
SinV_nsp2     CWAKALEPILDTAGIVLTGCQWSELFPQFADDKPHSAIYALDVICIKFFGMDLTSGLFSK 540
VEEV_nsp2     CWAKALVPVLKTAGIDMTTEQWNTVD-YFETDKAHSAEIVLNQLCVRFFGLDLDSGLFSA 535
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SFV_nsp2	PKVSLYYENN-----HWDNRPGGRMYGFNAATAARLEARHTFLKGQWHTGKQAVIAER	590
RRV_nsp2	QSVSLYYENN-----HWDNRPGGRMYGFNREVARKFEQRYPFRLRGKMDSGLQVNVPER	587
ONV_nsp2	PLISVYYADN-----HWDNRPGGKMFGFNPEVALMLEKKYPFTKGKWNINKQICITTR	590
SinV_nsp2	QSIPLTYHPADSARPVAHWDNSPGTRKYGYDHAIAAELSRRFPVFQ-LAGKGTQLDLQTG	599
VEEV_nsp2	PTVPLSIRNN-----HWDNSPSPNMYGLNKEVVRLSRRYPQLPRAVATGRVYDMNTG	588
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SFV_nsp2	KIQPLSVLDNVIPINRRLPHALVAEYKTVKGSRVVEWLVNKKVRGYHVLLVSEYNLALPRRR	650
RRV_nsp2	KVQPFNAECNILLNRRRLPHALVTSYQQCRGERVEWLLKKLPGYHLLLSEYNLALPHKR	647
ONV_nsp2	KVDEFNPETNIIIPANRRLPHSLVAEHHSVRGERMEWLVNKISGHMLLVSGHNLIIPTKR	650
SinV_nsp2	RTRVISAQHNLVPVNRNLPHALVPEYKEKQPGPVKKFLNQFKHHSVLVVSEEKIEAPRR	659
VEEV_nsp2	TLRNYDPRINLVPVNRRLPHALVLHNEHPQSDFSFVSKLKGRTVLVVG-EKLSVPGKK	647
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SFV_nsp2	VTWLSPLNVTGADRCYDLSLGLPADAGRFDLVFNINHTEFRIHHYQQCVDHAMKLQMLGG	710
RRV_nsp2	VFWIAPPHVSGADRIYDLDLGLPLNAGRYDLVFNINHTEYRTHHYQQCVDHSMKLQMLGG	707
ONV_nsp2	VTWVAPLGTRGADYTYNLELGLPATLGRYDLVINIHTPFRIHHYQQCVDHAMKLQMLGG	710
SinV_nsp2	IEWIAPIGIAGADKNYNLAFGFPPQA-RYDLVFINIGTKYRNHHFQQCEDHAATLKTLSR	718
VEEV_nsp2	VDWLS--DQPEATFRARLDLGIPGDVPKYDIVFINVRTPYKYHHYQQCEDHAIKLSMLTK	705
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SFV_nsp2	DALRLCLKPGG-ILMAYGYADKISEAVVSSLSRKFS SARVLRPDCVTSNTEVFLLFSNFD	769
RRV_nsp2	DSLHLL-PGGSLIRAYGYADRVSEMVVTALARKFSAFRVLRPACVTSNTEVFLLFTNFD	766
ONV_nsp2	DSLRLCLKPGGSLIRAYGYADRTSERVISVLGRKFRSSRALKPQCITSNTEMFLLFSRFD	770
SinV_nsp2	SALNCLNPGGTLVVKSYGYADRNSDVTALARKFVRVSAARPDCVSSNTEMYLIFRQLD	778
VEEV_nsp2	KACLHLNPGGTCVSI GYGYADRASESIIGAIARQFKFSRVCKPKSSHEETEVLVFIGYD	765
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SFV_nsp2	NGK-RPSTLHQMNTKLSAVYAGEAMHTAGC	798
RRV_nsp2	NGR-RAVTLHQANQRLSSMFACNGLHTAGC	795
ONV_nsp2	NGR-RNFTTHVMNQNNAVYAGLATR-AGC	798
SinV_nsp2	NSRTRQFTPHHLNCSVYEGTRDGVGA-	807
VEEV_nsp2	RKA-RTHNPKYKLSSTLTNIYTGSRLEAGC	794
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